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ALBERTO I. ROCA
Appl. No. 09/358,103
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79. The method of claim 73, wherein said aromatic amino acid is selected from the group consisting of phenylalanine, lysine, tyrosine, arginine and tryptophan.

80. The method of claim 74, wherein said aromatic amino acid is selected from the group consisting of tryptophan, tyrosine, phenylalanine, and histidine

81. The method of claim 69, wherein said non-aromatic amino acid is substituted at the position homologous to *E. coli* RecA residue 47 or 51, as represented by residue 8 or 12 of SEQ ID NO: 3.

82. The method of claim 81, wherein said aromatic amino acid is a tryptophan.

Remarks

I. Support for Amendments

Support for the foregoing amendments to the claims may be found throughout the specification and claims and originally filed. Specifically, support for the amendments can be found at pages 5-7; and page 15, line 20, through page 20, line 24. Accordingly, the present amendments do not add new matter, and their entry is respectfully requested.

II. Status of the Claims

By the foregoing amendments, claims 1 and 15 have been amended and claims 55-82 have been added. Upon entry of the foregoing amendments, claims **1-82** are pending in the current application application.

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III. The Rejection of the Claims Under 35 U.S.C. § 112, First Paragraph.

In the Office Action dated August 28, 2001, and reiterated in the telephonic interview of May 15, 2002, the Examiner has rejected claims 1-27 under 35 U.S.C. § 112, first paragraph, for allegedly lacking an adequate written description. Applicants respectfully traverse this rejection.

An adequate written description of a genus of biological molecules may be achieved by "a recitation of structural features common to the members of the genus." *Regents of the University of California v. Eli Lilly and Co.*, 199 F. 3d 1559, 1568-69 (Fed. Cir. 1997). The features relied upon to describe the claimed genus must be capable of distinguishing the members of the claimed genus from non-members. *Id.* In the present application the claimed proteins can be distinguished from all others by the presence of the MAW motif along with the presence of an appropriate mutation. As such, In Figure 1 of the present application Applicants have combined the sequences of RecA proteins from sixty-four prokaryotes, nine eukaryotes, one bacteriophage and one archea to disclose all possible amino acids at each position of the MAW motif. Further, Applicants have shown the potential amino acids that would be present in the claimed mutant enzymes. As such, one of ordinary skill in the art, using only these "common structural features" would easily be able to distinguish between those proteins that are encompassed by the claims and those that are not.

Applicants remind the Examiner that the written description requirement of 35 U.S.C. § 112, first paragraph is met if, "a person of ordinary skill in the art would have understood the inventor to have been in possession of the claimed invention at the time of filing...even if every nuance of the claims is not explicitly described in the specification." *In re Alton*, 76 F. 3d 1168, 1175 (Fed. Cir. 1996). It is clear that one of ordinary skill in the art, in light of the sequence

information disclosed in the specification, would have understood the Applicants to have been in possession of the invention, which has been defined by the United States Supreme Court as "a *concept* that is complete." *Pfaff v. Wells Electronics, Inc.* 525 U.S. 55, 66 (1998) Therefore, the rejection of claims 1-27 under 35 U.S.C. § 112, first paragraph is improper. Reconsideration and withdrawal of this rejection are respectfully requested.

IV. The Rejection of the Claims Under 35 U.S.C. § 112, Second Paragraph.

In the Office Action dated August 28, 2001, and reiterated in the telephonic interview of May 15, 2002, the Examiner has rejected claims 1-27 under 35 U.S.C. § 112, second paragraph for allegedly being indefinite. Applicants respectfully traverse this rejection.

The Examiner asserts that the phrases, "mutant RecA homolog", "MAW motif", and "homologous to the *E. coli* MAW motif" are not known and not defined in the specification. Applicants respectfully traverse this rejection.

It is clearly established that, "whether a claim is invalid for indefiniteness depends on whether those skilled in the art would understand the scope of the claim when the claim is read in light of the specification." *North American Vaccine, Inc. v. American Cyanamid Co.*, 7 F. 3d 1571 (Fed. Cir. 1993). At page 1, line 17; and page 5, lines 20-21 that phrase "MAW motif" has been defined, for example, as "amino acid residues 40 to 65 in the *Escherichia coli* (*E. coli*) RecA protein (SEQ ID NO: 1) and the homologs of this structure in other proteins." At page 5, line 22, through page 5, line 7, the phrase "RecA homolog protein" has been defined, for example, as an *E. coli* protein having the MAW motif or homologs thereof. Further, at page 6, lines 15-17, the phrase "RecA homolog protein mutant" has been defined, for example, as an *E.*

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coli RecA protein, or a bacterial, eukaryotic, archael or viral homolog thereof, in which the naturally occurring MAW motif has been modified by one or more such replacements of amino acid residues. As such, these definitions clearly relate the intended meaning of the terms so that one of ordinary skill in the art would readily recognize what is meant by the phrase "mutant RecA protein homolog comprising a MAW motif homologous to the *E. coli* MAW motif." Moreover, these phrases are in common usage in the field of molecular biology and biochemistry and one of ordinary skill in the art would immediately appreciate their intended meaning.

As such, the rejection of claims 1-27 under 27 U.S.C. § 112, second paragraph is improper. Reconsideration and withdrawal of this rejection are respectfully requested.

V. Conclusion

All of the stated grounds of objection and rejection have been properly traversed. Applicants therefore respectfully request that the Examiner reconsider all presently outstanding rejections and that they be withdrawn.

Applicants believe that the present application is in condition for allowance. If the Examiner believes, for any reason, that personal communication will expedite prosecution of this application, the Examiner is invited to telephone the undersigned at the number provided.

Respectfully submitted,

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Date: _____

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Copy of claims as amended

1. In an *E. coli* RecA protein or a protein having a MAW motif homologous to the *E. coli* MAW motif, a RecA homolog protein mutant, wherein a naturally occurring amino acid residue located within the protein's homolog of *E. coli* residues 40 to 65, inclusive, shown in SEQ ID NO: 3, is replaced with a replacement amino acid residue which is volumetrically larger than the replaced amino acid residue.

15. In an *E. coli* RecA protein or a protein having a MAW motif homologous to the *E. coli* MAW motif, a RecA homolog protein mutant, wherein a naturally occurring amino acid residue located within the protein's homolog of *E. coli* residues 40 to 65, shown in SEQ ID NO: 3, inclusive, but excluding the protein's homolog of *E. coli* residues 47 and 51 (SEQ ID NO: 3, residues 8 and 12), is replaced with a replacement aromatic amino acid residue.

55. A method of generating a mutant RecA protein having enhanced DNA binding activity, comprising substituting an amino acid in the MAW motif of the wildtype RecA protein with a volumetrically larger amino acid.

56. The method of claim 55, wherein said volumetrically larger amino acid is substituted at the position homologous to *E. coli RecA* residue 43, as represented by residue 4 of SEQ ID NO: 3.

57. The method of claim 55, wherein said volumetrically larger amino acid is substituted at the position homologous to *E. coli RecA* residue 52, as represented by residue 13 of SEQ ID NO: 3.

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58. The method of claim 55, wherein said volumetrically larger amino acid is substituted at the position homologous to *E. coli RecA* residue 53, as represented by residue 14 of SEQ ID NO: 3.

59. The method of claim 55, wherein said volumetrically larger amino acid is substituted at the position homologous to *E. coli RecA* residue 54, as represented by residue 15 of SEQ ID NO: 3.

60. The method of claim 55, wherein said volumetrically larger amino acid is substituted at the position homologous to *E. coli RecA* residue 55, as represented by residue 16 of SEQ ID NO: 3.

61. The method of claim 55, wherein said volumetrically larger amino acid is substituted at the position homologous to *E. coli RecA* residue 59, as represented by residue 20 of SEQ ID NO: 3.

62. The method of claim 55, wherein said volumetrically larger amino acid is selected from the group consisting of phenylalanine, lysine, tyrosine, arginine and tryptophan.

63. The method of claim 56, wherein said volumetrically larger amino acid is selected from the group consisting of phenylalanine, lysine, tyrosine, arginine and tryptophan.

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64. The method of claim 57, wherein said volumetrically larger amino acid is selected from the group consisting of phenylalanine, lysine, tyrosine, arginine and tryptophan.

65. The method of claim 58, wherein said volumetrically larger amino acid is selected from the group consisting of phenylalanine, lysine, tyrosine, arginine and tryptophan.

66. The method of claim 59, wherein said volumetrically larger amino acid is selected from the group consisting of phenylalanine, lysine, tyrosine, arginine and tryptophan.

67. The method of claim 60, wherein said volumetrically larger amino acid is selected from the group consisting of phenylalanine, lysine, tyrosine, arginine and tryptophan.

68. The method of claim 61, wherein said volumetrically larger amino acid is selected from the group consisting of phenylalanine, lysine, tyrosine, arginine and tryptophan.

69. A method of generating a mutant RecA protein having enhanced DNA binding activity, comprising substituting a non-aromatic amino acid in the MAW motif of the wildtype RecA protein with an aromatic amino acid.

70. The method of claim 69, wherein said non-aromatic amino acid is substituted at the position homologous to *E. coli RecA* residue 40, as represented by residue 1 of SEQ ID NO: 3.

71. The method of claim 69, wherein said non-aromatic amino acid is substituted at the position homologous to *E. coli RecA* residue 42, as represented by residue 3 of SEQ ID NO: 3.

72. The method of claim 69, wherein said non-aromatic amino acid is substituted at the position homologous to *E. coli RecA* residue 44, as represented by residue 5 of SEQ ID NO: 3.

73. The method of claim 69, wherein said non-aromatic amino acid is substituted at the position homologous to *E. coli RecA* residue 50, as represented by residue 11 of SEQ ID NO: 3.

74. The method of claim 69, wherein said non-aromatic amino acid is substituted at the position homologous to *E. coli RecA* residue 56, as represented by residue 17 of SEQ ID NO: 3.

75. The method of claim 69, wherein said aromatic amino acid is selected from the group consisting of tryptophan, tyrosine, phenylalanine, and histidine.

76. The method of claim 70, wherein said aromatic amino acid is selected from the group consisting of tryptophan, tyrosine, phenylalanine, and histidine.

77. The method of claim 71, wherein said aromatic amino acid is selected from the

group consisting of tryptophan, tyrosine, phenylalanine and histidine..

78. The method of claim 72, wherein said aromatic amino acid is selected from the group consisting of phenylalanine, lysine, tyrosine, arginine and tryptophan.

79. The method of claim 73, wherein said aromatic amino acid is selected from the group consisting of phenylalanine, lysine, tyrosine, arginine and tryptophan.

80. The method of claim 74, wherein said aromatic amino acid is selected from the group consisting of tryptophan, tyrosine, phenylalanine, and histidine

81. The method of claim 69, wherein said non-aromatic amino acid is substituted at the position homologous to *E. coli* RecA residue 47 or 51, as represented by residue 8 or 12 of SEQ ID NO: 3.

82. The method of claim 81, wherein said aromatic amino acid is a tryptophan.